

1647



1600

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/005,318E

DATE: 07/30/2002

TIME: 15:12:02

Input Set : A:\Epi3004b.app

Output Set: N:\CRF3\07302002\I005318E.raw

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AUG 06 2002

TECH CENTER 1600/2900

3 <110> APPLICANT: HEIN, MICH B.
 4 HIATT, ANDREW C.
 5 FITCHEN, JOHN H.
 7 <120> TITLE OF INVENTION: NOVEL EPITHELIAL TISSUE TARGETING AGENT
 9 <130> FILE REFERENCE: EPI3004B
 11 <140> CURRENT APPLICATION NUMBER: 09/005,318E
 12 <141> CURRENT FILING DATE: 1998-01-09
 14 <150> PRIOR APPLICATION NUMBER: 08/782,481
 15 <151> PRIOR FILING DATE: 1997-01-10
 17 <150> PRIOR APPLICATION NUMBER: 09/005,167
 18 <151> PRIOR FILING DATE: 1998-01-09
 20 <160> NUMBER OF SEQ ID NOS: 113
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 137
 26 <212> TYPE: PRT
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys Ala
 31 1 5 10 15
 33 Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu Asp
 34 20 25 30
 36 Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg Glu
 37 35 40 45
 39 Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Pro Val Tyr His
 40 50 55 60
 42 Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu Asp
 43 65 70 75 80
 45 Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp Ser
 46 85 90 95
 48 Ala Thr Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Ala
 49 100 105 110
 51 Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr Ala
 52 115 120 125
 54 Leu Thr Pro Asp Ala Cys Tyr Pro Asp
 55 130 135
 58 <210> SEQ ID NO: 2
 59 <211> LENGTH: 135
 60 <212> TYPE: PRT
 61 <213> ORGANISM: Mus sp.
 63 <400> SEQUENCE: 2
 64 Gln Asp Glu Asn Glu Arg Ile Val Val Asp Asn Lys Cys Lys Cys Ala
 65 1 5 10 15

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67 Arg Ile Thr Ser Arg Ile Ile Pro Ser Ala Glu Asp Pro Ser Gln Asp
68           20           25           30
70 Ile Val Glu Arg Asn Val Arg Ile Ile Val Pro Leu Asn Ser Arg Glu
71           35           40           45
73 Asn Ile Ser Asp Pro Thr Ser Pro Met Arg Thr Lys Pro Val Tyr His
74           50           55           60
76 Leu Ser Asp Leu Cys Lys Lys Cys Asp Thr Thr Glu Val Glu Leu Glu
77 65           70           75           80
79 Asp Gln Val Val Thr Ala Ser Gln Ser Asn Ile Cys Asp Ser Asp Ala
80           85           90           95
82 Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Asn Arg Val
83           100          105          110
85 Lys Leu Ser Tyr Arg Gly Gln Thr Lys Met Val Glu Thr Ala Leu Thr
86           115          120          125
88 Pro Asp Ser Cys Tyr Pro Asp
89           130          135
92 <210> SEQ ID NO: 3
93 <211> LENGTH: 137
94 <212> TYPE: PRT
95 <213> ORGANISM: Oryctolagus cuniculus
97 <400> SEQUENCE: 3
98 Asp Asp Glu Ala Thr Ile Leu Ala Asp Asn Lys Cys Met Cys Thr Arg
99 1           5           10           15
101 Val Thr Ser Arg Ile Ile Pro Ser Thr Glu Asp Pro Asn Glu Asp Ile
102           20           25           30
104 Val Glu Arg Asn Ile Arg Ile Val Val Pro Leu Asn Asn Arg Glu Asn
105           35           40           45
107 Ile Ser Asp Pro Thr Ser Pro Leu Arg Arg Asn Pro Val Tyr His Leu
108           50           55           60
110 Ser Asp Val Cys Lys Lys Cys Asp Pro Val Glu Val Glu Leu Glu Asp
111 65           70           75           80
113 Gln Val Val Thr Ala Thr Gln Ser Asn Ile Cys Asn Glu Asp Asp Gly
114           85           90           95
116 Val Pro Glu Thr Cys Tyr Met Tyr Asp Arg Asn Lys Cys Tyr Thr Thr
117           100          105          110
119 Met Val Pro Leu Arg Tyr His Gly Glu Thr Lys Met Val Gln Ala Ala
120           115          120          125
122 Leu Thr Pro Asp Ser Cys Tyr Pro Asp
123           130          135
126 <210> SEQ ID NO: 4
127 <211> LENGTH: 136
128 <212> TYPE: PRT
129 <213> ORGANISM: Bos sp.
131 <400> SEQUENCE: 4
132 Glu Asp Glu Ser Thr Val Leu Val Asp Asn Lys Cys Gln Cys Val Arg
133 1           5           10           15
135 Ile Thr Ser Arg Ile Ile Arg Asp Pro Asp Asn Pro Ser Glu Asp Ile
136           20           25           30
138 Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Thr Arg Glu Asn

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139          35          40          45
141 Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Glu Pro Lys Tyr Asn Leu
142          50          55          60
144 Ala Asn Leu Cys Lys Lys Cys Asp Pro Thr Glu Ile Glu Leu Asp Asn
145 65          70          75          80
147 Gln Val Phe Thr Ala Ser Gln Ser Asn Ile Cys Pro Asp Asp Asp Tyr
148          85          90          95
150 Ser Glu Thr Cys Tyr Thr Tyr Asp Arg Asn Lys Cys Tyr Thr Thr Leu
151          100          105          110
153 Val Pro Ile Thr His Arg Gly Val Thr Arg Met Val Lys Ala Thr Leu
154          115          120          125
156 Thr Pro Asp Ser Cys Tyr Pro Asp
157          130          135
160 <210> SEQ ID NO: 5
161 <211> LENGTH: 119
162 <212> TYPE: PRT
163 <213> ORGANISM: Rana sp.
165 <220> FEATURE:
166 <221> NAME/KEY: MOD_RES
167 <222> LOCATION: (47)
168 <223> OTHER INFORMATION: Variable amino acid
170 <220> FEATURE:
171 <221> NAME/KEY: MOD_RES
172 <222> LOCATION: (88)..(89)
173 <223> OTHER INFORMATION: Variable amino acid
175 <220> FEATURE:
176 <221> NAME/KEY: MOD_RES
177 <222> LOCATION: (91)
178 <223> OTHER INFORMATION: Variable amino acid
180 <400> SEQUENCE: 5
181 Glu Gln Glu Tyr Ile Leu Ala Asn Asn Lys Cys Lys Cys Val Lys Ile
182 1          5          10          15
184 Ser Ser Arg Phe Val Pro Ser Thr Glu Arg Pro Gly Glu Glu Ile Leu
185          20          25          30
W--> 187 Glu Arg Asn Ile Gln Ile Thr Ile Pro Thr Ser Ser Arg Met Xaa Ile
188          35          40          45
190 Ser Asp Pro Tyr Ser Pro Leu Arg Thr Gln Pro Val Tyr Asn Leu Trp
191          50          55          60
193 Asp Ile Cys Gln Lys Cys Asp Pro Val Gln Leu Glu Ile Gly Gly Ile
194 65          70          75          80
W--> 196 Pro Val Leu Ala Ser Gln Pro Xaa Xaa Ser Xaa Pro Asp Asp Glu Cys
197          85          90          95
199 Tyr Thr Thr Glu Val Asn Phe Lys Lys Lys Val Pro Leu Thr Pro Asp
200          100          105          110
202 Ser Cys Tyr Glu Tyr Ser Glu
203          115
206 <210> SEQ ID NO: 6
207 <211> LENGTH: 128
208 <212> TYPE: PRT

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209 <213> ORGANISM: Lumbricus sp.

211 <400> SEQUENCE: 6

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212 Asn Lys Cys Met Cys Thr Arg Val Thr Ala Arg Ile Arg Gly Thr Arg
213      1          5          10          15
215 Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Tyr Ile Arg Ile Asn Val
216      20          25          30
218 Pro Leu Lys Asn Arg Gly Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg
219      35          40          45
221 Asn Gln Pro Val Tyr His Leu Ser Pro Ser Cys Lys Lys Cys Asp Pro
222      50          55          60
224 Tyr Glu Asp Gly Val Val Thr Ala Thr Glu Thr Asn Ile Cys Tyr Pro
225      65          70          75          80
227 Asp Gln Gly Val Pro Gln Ser Cys Arg Asp Tyr Cys Pro Glu Leu Asp
228      85          90          95
230 Arg Asn Lys Cys Tyr Thr Val Leu Val Pro Pro Gly Tyr Thr Gly Glu
231      100          105          110
233 Thr Lys Met Val Gln Asn Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
234      115          120          125

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237 <210> SEQ ID NO: 7

238 <211> LENGTH: 421

239 <212> TYPE: DNA

240 <213> ORGANISM: Artificial Sequence

242 <220> FEATURE:

243 <221> NAME/KEY: CDS

244 <222> LOCATION: (1)..(414)

246 <220> FEATURE:

247 <221> NAME/KEY: sig_peptide

248 <222> LOCATION: (1)..(6)

250 <220> FEATURE:

251 <221> NAME/KEY: mat_peptide

252 <222> LOCATION: (7)..(414)

254 <220> FEATURE:

255 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 256 nucleotide sequence

258 <400> SEQUENCE: 7

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259 gat cag gaa gat gaa cgt att gtt ctg gtt gac aac aag tgc aag tgt      48
260 Asp Gln Glu Asp Glu Arg Ile Val Leu Val Asp Asn Lys Cys Lys Cys
261      -1  1          5          10
263 gct cgt att act tct aga atc atc cgt agc tca gag gac cca aat gaa      96
264 Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser Ser Glu Asp Pro Asn Glu
265      15          20          25          30
267 gat ata gtc gaa cgt aac atc cgt atc atc gtc cca ctg aat aac cgg      144
268 Asp Ile Val Glu Arg Asn Ile Arg Ile Ile Val Pro Leu Asn Asn Arg
269      35          40          45
271 gag aat atc tca gat cct aca agt ccg ttg cgc aca cgc ttc gta tac      192
272 Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu Arg Thr Arg Phe Val Tyr
273      50          55          60
275 cac ctg tca gat ctg tgt aag aag tgt gat cca aca gag gta gag ctg      240
276 His Leu Ser Asp Leu Cys Lys Lys Cys Asp Pro Thr Glu Val Glu Leu

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DATE: 07/30/2002

PATENT APPLICATION: US/09/005,318E

TIME: 15:12:02

Input Set : A:\Epi3004b.app

Output Set: N:\CRF3\07302002\I005318E.raw

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277          65          70          75
279 gac aat cag ata gtc act gcg act caa agc aac att tgc gat gag gac 288
280 Asp Asn Gln Ile Val Thr Ala Thr Gln Ser Asn Ile Cys Asp Glu Asp
281          80          85          90
283 agc gct aca gaa acc tgc agc acc tac gat agg aac aaa tgc tac acg 336
284 Ser Ala Thr Glu Thr Cys Ser Thr Tyr Asp Arg Asn Lys Cys Tyr Thr
285 95          100          105          110
287 gcc gtg gtt ccg ctc gtg tat ggt gga gag aca aaa atg gtg gaa act 384
288 Ala Val Val Pro Leu Val Tyr Gly Gly Glu Thr Lys Met Val Glu Thr
289          115          120          125
291 gcc ctt acg ccc gat gca tgc tat ccg gac tgaattc 421
292 Ala Leu Thr Pro Asp Ala Cys Tyr Pro Asp
293          130          135
297 <210> SEQ ID NO: 8
298 <211> LENGTH: 215
299 <212> TYPE: DNA
300 <213> ORGANISM: Artificial Sequence
302 <220> FEATURE:
303 <221> NAME/KEY: CDS
304 <222> LOCATION: (1)..(213)
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
308     nucleotide sequence
310 <400> SEQUENCE: 8
311 gat cag aag tgc aag tgt gct cgt att act tct aga atc atc cgt agc 48
312 Asp Gln Lys Cys Lys Cys Ala Arg Ile Thr Ser Arg Ile Ile Arg Ser
313 1          5          10          15
315 tca gag gac cca aat gaa gat ata gtc gaa cgt aac atc cgt atc atc 96
316 Ser Glu Asp Pro Asn Glu Asp Ile Val Glu Arg Asn Ile Arg Ile Ile
317          20          25          30
319 gtc cca ctg aat aac cgg gag aat atc tca gat cct aca agt ccg ttg 144
320 Val Pro Leu Asn Asn Arg Glu Asn Ile Ser Asp Pro Thr Ser Pro Leu
321          35          40          45
323 cgc aca cgc ttc gta tac cac ctg tca gat ctg tgt aag aag gat gag 192
324 Arg Thr Arg Phe Val Tyr His Leu Ser Asp Leu Cys Lys Lys Asp Glu
325          50          55          60
327 gac agc gct aca gaa acc tgc tg 215
328 Asp Ser Ala Thr Glu Thr Cys
329 65          70
333 <210> SEQ ID NO: 9
334 <211> LENGTH: 140
335 <212> TYPE: DNA
336 <213> ORGANISM: Artificial Sequence
338 <220> FEATURE:
339 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
340     nucleotide sequence
342 <400> SEQUENCE: 9
343 ctagaatcat ccgtagctca gaggacccaa atgaagatat agtcgaacgt aacatccgta 60
344 tcacgtccc actgaataac cgggagaata tctcagatcc tacaagtccg ttgcgcacac 120

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/005,318E

DATE: 07/30/2002
TIME: 15:12:03

Input Set : A:\Epi3004b.app
Output Set: N:\CRF3\07302002\I005318E.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; Xaa Pos. 47,88,89,91

VERIFICATION SUMMARY

DATE: 07/30/2002

PATENT APPLICATION: US/09/005,318E

TIME: 15:12:03

Input Set : A:\Epi3004b.app

Output Set: N:\CRF3\07302002\I005318E.raw

L:187 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:32
L:196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:80